# BIBLICAL CREATION

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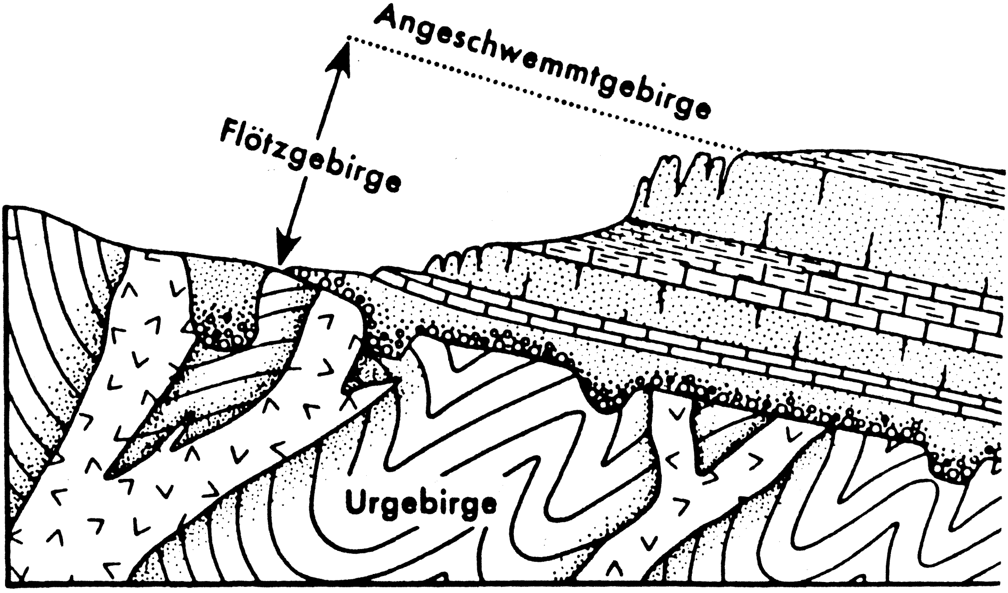

Geological cross-section of the rocks studied by Werner in Saxony showing the relationship between his three major divisions of the stratigraphic record. A major unconformity exists between the Urgebirge and the Flötzgebirge.

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# Guest Editorial: Sacred and Secular?

For generations Christians in science have tacitly supported a strategy that fundamentally compromises the Christian faith. In life, if not from lip, we have commuted between two worlds: a *spiritual world* under God's word, of church activities, evangelism, Bible study and personal devotion and ethics and a *material world* governed by the autonomous and inexorable laws of science. (Where, in this duality, to put such realms as those of society, law, politics, art, economics, literature and leisure, is a tricky problem we have been happy to leave to others!).

Our tacit commitment to this two-worlds perspective is betrayed in the things we fail to see and in those we see too well. We in Britain were well-satisfied with the 1944 Education Act when it affirmed a place for religion in schools. Yet that Act was a disaster for Christian education. Religion was given a narrow slot in the school timetable on the momenteous assumption that it has no relevance to the rest of the school curriculum — and that 'rest' includes the bulk of which is significant for everyday life. Worse still, faith was excluded even from the religious slot and relegated to a private sphere of personal life and church attendance. To this day, Religious Education is viewed as a matter of passing on objective information without passion or vision. We have accepted a divorce of faith from knowledge and lost our Christian birthright in the process. Belatedly we now accept that our state schools are propagating secular humanism, yet our understanding of what this means remains blinkered.

Our discussions of the secular influence in education focus almost exclusively on issues of 'religion' (e.g. the problems of multifaith RE) or of 'morality' (e.g. the showing of video 'nasties' in schools; teaching homosexualism as a valid lifestyle; teaching sex as a matter of 'plumbing' and some social consequences). But the secular world-view underlies the whole state approach to education and moulds the content of *every* subject. On every hand our children are being indoctrinated against a Christian understanding of the world and of the issues of life.

In the sciences are our children learning about a cold factual world of matter functioning according to inherent ('natural') laws, from which man developed by chance and over which he must gain technological control? Or are they learning about a created order, structured by and responding to God's word of power, a world in which the sciences as well as techology are obedient or disobedient responses to His will?

Is history merely a matter of seemingly purposeless dates and events or a story of civilization progressing from primitive abominations to a golden future of warless, planned democracy? Does it equip our children to understand the spirits of our age, their nature, origin and effectiveness? Does it highlight the antithesis between the children of light and those of darkness? Is the pageant of history seen in the light of God's will for cultural development?

Do the humanities presume that men are rational beings who order their society, write their literature and create their arts according to the passing standards upheld in their particular culture? Will God's norms and ordinances for society (state, family, marriage etc.) be clarified so that our children can gain insight into the deformations around them and be enabled to support those seeking to reform what belief has distorted against the very grain of creation? Will they understand that self-fulfilment and the highest fulfilment of family and community life lie in obedient harmony with God's laws? Will the literature they read be 'twaddle' (or worse!) or will they be introduced to authors who think deeply and sensitively and who express themselves well? Are they taught in language lessons to express themselves truthfully, appropriately, clearly, considerately, concisely, beautifully, justly? Can they discern the spirit behind the art in magazines, on TV, on billboards?

If we believe it is right to leave our children in state schools to be 'salt' and 'light', then where do they learn a Christian perspective? Do we make time for it at home or in the church programme? Do our children grow up knowing their relationships to God's world, feeling at home in it, enjoying what is to be enjoyed, discerning the good and the evil, understanding it, *knowing it?* Where do they learn these things? Anywhere?

The problem is that so many grow up as Christians *and* doctors, nurses, farmers, farm or factory workers, teachers, musicians etc., but so few become *Christian* doctors, farmers or musicians. We may even become missionaries, but still fail to develop, or perhaps never even consider, a Christian perspective and alternative in agriculture, medicine or music. We must not, dare not, ignore our folly, but repent and bring all of life under the lordship of Christ.

**Arthur Jones**

# CREATIONISM IN JAPAN

## David J. Tyler

The opening verse of the Bible establishes the distinction between God and the physical world. This verse refutes the idea that all reality is basically 'one' — as pantheists and others suggest. The sovereign God is not to be equated and identified with the results of his handiwork. This understanding is fundamental to the Christian world-view, but is lacking in many of the world religions. It is absent in Japan, where the two dominant religions are Shintoism and Buddhism. In this country, Christian references to 'God' are commonly reinterpreted and misunderstood by those who hear the message.

Shintoism is associated with the gods of Japan, with ancestor worship and with many patriotic ceremonies. As a consequence, it promotes a nationalistic spirit among the Japanese, leading to a sense of superiority and motivating people to achieve success.

Buddhism, on the other hand, is more relevant to the cycle of birth, marriage and death and it dominates these occasions. Japanese people appear to adhere happily to both religions as the need arises. (Indeed, syncretism extends even to Hinduism. In one Buddhist temple, that of Sanjusangendo in Kyoto, 30 Hindu gods and spirits guard the 1001 Buddhist images!)

The nationalistic spirit of the Japanese people provides the rationale for their dramatic and chequered history and markedly hierarchical social structure. After the Feudal Period, when they lived in almost complete isolation from the outside world, their sense of superiority expressed itself in a desire to dominate other nations. A whole series of military enterprises ensued — culminating in World War II. Of this period, Griffiths says:

> "It emerges from all this that the person really responsible for the Pacific War was Charles Darwin! His doctrine of the survival of the fittest and the struggle for existence was the kind of idea which could so easily be grafted onto the Japanese myth of superiority guaranteed by the Shinto gods of Japan. So the Shinto religion became a powerful weapon in the hands of the militarists, who deliberately exploited it in the interests of nationalism. A gradual build-up of military power took place until they were ready to defeat first China, then Russia, then China again, and finally Britain and America." (1, p.18).

The mix of Buddhism, Shintoism and nationalism has contributed to a deeply-felt aversion to Christ and the gospel of salvation. The biblical analysis of man's need, his relationship to God and the way of reconciliation is one which has very few points of contact with the Japanese world-view. Griffiths' book portrays something of the hardness of gospel work in Hokkaido, which is representative of similar situations experienced throughout Japan.

The problem of communication must be faced — how is it possible for Christians to establish meaningful communication with people who possess a radically different world-view? Monism, idealism and pantheism are fundamentally at variance with the Christian commitment to pluralism, realism and Theism.

Somehow, a challenge must be made to a fundamentally false world-view. Christians involved with the Japan Creation Science Society have found that the doctrine of creation is directly relevant to this problem. Japanese people have no concept of divine immanence and do not relate easily to Christian testimony on this topic. However, they do have a concept of a transcendent creator god — as the powerful Sun-god of Japan still has a subconscious influence. Consequently, many Japanese are intrigued by the idea that evolution is not true and that our origins must be traced back to a transcendent creator. The doctrine of creation presents a fundamental challenge to the Japanese world-view, and it confronts the widespread relativism which characterises their collective religious mind. It is interesting that Japanese people thinking about creation soon make the connection between God as Creator and God as Judge. If we are created by God, then we are responsible to him and the self-centred life is recognised to be offensive and wrong.

The Japanese Creation Science Society has developed recently from the Bible and Science Press. This publishing group has been led by Dr. Masami Usami, a medical doctor, and five trustees. They have published a number of translations of books, including 'The scientific case for creation' by Henry Morris, 'From evolution to creation' by Gary Parker, 'How did it all begin?' by John Whitcomb, and 'Bone of Contention' by Sylvia Baker. Other translations are in progress. A monthly magazine is produced for subscribers which includes articles by Dr. Usami and translations of selected 'Impact' articles published by the Institute for Creation Research, California.

The importance of the doctrine of creation in reorienting the world-view of men and women is something not to be restricted to Japan. One example, from another nation and another culture, comes from China. The testimony of a mainland Chinese Christian intellectual was reported recently in the newsletter 'Pray for China' (2):

> 'Our Chinese Christian friend said that he often started to interest intellectuals in the Gospel by talking about the origin of the universe. He would show that by modern theories of probability it was impossible that an ordered universe could have evolved out of chaos, that life could

> have emerged spontaneously from dead matter, or that intelligence could have evolved by sheer chance. He could then point his enquirer to God, who was the divine Mind and Creator of the universe.
>
> Another approach he uses is to ask the intellectual — what is man? Is he merely an animal, or even merely a thinking animal? Eventually he would point out that man had a conscience, able to judge between good and evil. This moral sense could only come from God, the ultimate arbiter of right and wrong.
>
> Once having caused his enquirer to face up to realities concerning himself, it was not too difficult to go on to discuss the question of sin and the problem of man's broken relationship with his Creator. He could then talk about Jesus, the cross and the way of salvation. However, if he had plunged right in at the beginning with the way of salvation, he would probably have alienated his unbelieving friend.'

The concept of 'creation evangelism' is appropriate in many parts of the world — including countries where humanism holds sway. If Christians in Britain would stop treating the creation/evolution issue as an 'academic' and unfruitful controversy, and start seeing it in terms of conceptual frameworks and world-views, then real progress could be made. Perhaps here we can learn something from the experience of our Japanese brethren.

The Japanese Creation Science Society can be contacted at 1-4-41 Kaminito, Mito Shi, Ibaraki Ken, Japan 310.

### Acknowledgements

Conversation and correspondence with Carlton Elkins, a trustee of the Bible and Science Press, has been invaluable in the preparation of this article.
The quotation from 'Pray for China' is reproduced by permission of Christian Communications Ltd.

### References

(1) Griffiths, M.C. *Take off your shoes*. London: OMF. (1971).
(2) The Gospel for China's intellectuals. *Pray for China*. (1984, Sept-Oct. No. 62 pp 4-5.)

**Biblical Creation 7:20**

# GENES - CREATED BUT EVOLVING

## Chris Darnbrough

### Summary

Genetic mechanisms causing evolutionary change are described, and shown to be a reasonable basis for a limited evolutionary view of origins. The implications of the *de novo* creation of genes and genomes are discussed and the effects of evolutionary processes on the creation are considered. It is concluded that the evolution of originally created genes is a good model for the origin of modern genomes and observed genetic phenomena.

### Introduction

To the convinced anti-evolutionist the ideas put forward in this paper may appear unconventional and even heretical. The author is a Biblical creationist who is also a molecular biologist, and constantly sees vast amounts of biological data being interpreted within an evolutionary framework. Such interpretations, although usually superfluous, are not always misleading or erroneous. Evolution at the level of genes and molecules, as process, is a reality which can be studied experimentally and which can bring about major genetic change in gene pools and natural populations. Such a view does not imply any agreement with Evolutionism, either as a model for organic origins or as a philosophy, nor does it lead to a theistic evolutionary position.

In the beginning, when God created living things, He necessarily created genes, since organic life and all its characteristics are entirely determined by and dependent upon the genes that encode it. It is true also that all life is sustained by God, but that belief does not affect the way in which we as scientists carry out experiments and interpret them — though it may affect the ethics of our science — so long as we examine *process*. Thus the Bible-believing Christian has no grounds on which to reject the validity of scientific methods in studying evolutionary processes. To accept the extrapolation of that process back to Genesis 1.1, however, is to deny the Word of God which tells us that the creation process was different.

The opening chapters of Genesis do not tell us anything about process.Thus we are unable, for instance, to make scientific statements about the duration of the six creation days, but we are able to deduce that God planned, designed and created *ex nihilo*, a universe that was 'very good'. Combined with what we know about the nature of God, we may then work out the essential characteristics of the living world as newly created, at the moment when Adam first stood, as a mature but newly formed being, in the Garden prepared for him. Until that moment, we may understand what God has revealed to us by faith alone (Hebrews 11.3), and not in scientific terms. Since that moment the universe has been subject to physical laws of which we may eventually have complete understanding.

From the moment of his creation Adam, and all nature with him, has been evolving in some sense. Creation was a finished act of God, but evolution is a continuing process of natural law.

This paper seeks to discuss the effects of evolutionary processes on a created living world, at the level of genes and genetics. The scientific issues dealt with are necessarily highly technical, and are given in the text in somewhat simplified form. Selected topics are amplified, with examples and references, in the footnotes.[1]

## Starting points

The Word of God is the only valid justification for a creationist view of origins. The impossibility of a chemical origin of life is the only convincing basis for rejecting the evolutionary model of origins[2], but we must beware of assuming that rejection of chemical evolution necessarily leads to a creationist position. However, for the evolutionist chemical evolution is an inescapable necessity, despite its lack of any experimental or theoretical basis. We do not need to enter into details here[2]. The problem, apart from the chemistry itself, which does not work, is really a genetic one. Figure 1 expresses simply that a living cell is a bounded, self-replicating system containing structures and information, in which

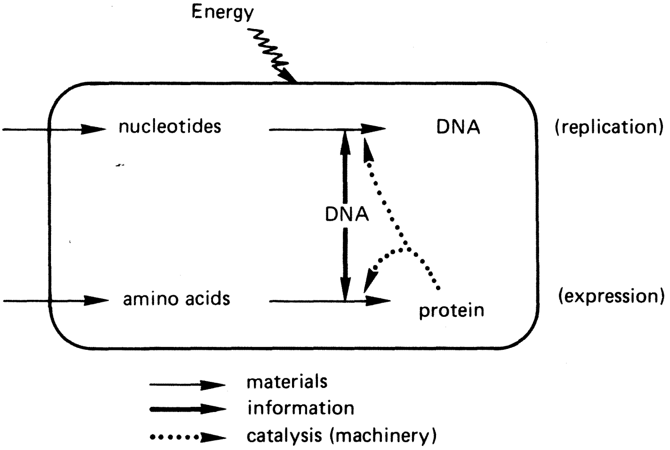


*Figure 1. Essential characteristics of organic life.*

the information (DNA sequences) is expressed by means of structures (protein molecules) which are themselves products of the expression of that information. DNA outside the context of the cellular machinery which decodes it, is an inert chemical. Information implies context, and the context for genetic information is a consistent genetic code and appropriate transcription and translation mechanisms.

No credible model exists to explain the origin of such a system by naturalistic mechanisms. Only intelligent design (creation) is able to generate a living system.

## Organic evolution?

If we allow the assumption that a primordial living cell did somehow emerge from the rather dilute primeval soup, is it possible to progress further? The question first needs to be restated in genetic terms: is it possible, by random processes, to achieve an increase, sustained over evolutionary time, in the informational complexity of a genome or population gene pool? This is not to say that, for instance, man is more highly evolved than amoeba, but is simply to recognise the fact that man is, by several orders of magnitude, genetically more complex than amoeba. Evolution as a theory of origins requires that the total informational complexity of individual genomes and of the entire biosphere has increased steadily through evolutionary time, and presumably continues to increase. Information here means a sequence of bases in DNA which in the context of the cellular translation machinery, confers some selectable phenotype on the cell or organism.

The answer to the question is not a decisive Yes, but neither can it be a simple No. Of the few perennially quoted examples which appear to support the evolutionary view, only the peppered moth is readily explained away by natural selection rather than by the appearance of novel genetic information. It would be foolish to assert that genes for antibiotic resistance carried on bacterial plasmids were specially created; in bacteria it is certain that selectable phenotypes can arise by random modification of existing genes[3].

At this level the evolutionist's position is a reasonable one, and it is likely that well understood genetic mechanisms are capable of producing much more evolutionary change than most creationists are prepared to consider possible. Nevertheless, the limits of evolutionary change must remain a matter of speculation and argument. It is most unlikely that genetic mechanisms can account for transitions such as that from reptiles to birds, but it is likely that evolution occurs beyond the bounds of what is commonly called micro-evolution. The type of experiment required to demonstrate such processes is somewhat time-consuming[4].

## How evolution works[5]

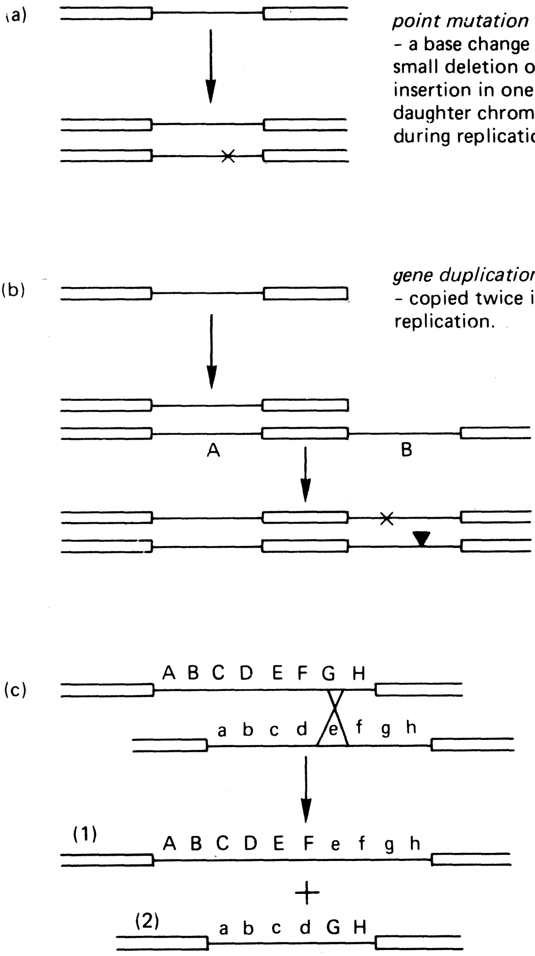
Recent research in molecular genetics has revealed that the genome (DNA complement) of an organism is not so fixed as was once believed by even neo-Darwinists, who once relied on random mutation events as the major source of selectable genetic variation. It is now apparent that cells contain many normal mechanisms responsible for modifying, rearranging and translocating genes as aspects of essential cellular functions. DNA may also be transferred from one organism to another, and every mammalian genome contains much DNA integrated into the chromosomes which is of viral origin but related to cellular genes.

## Mutation and natural selection - microevolution?

The vast majority of point mutations, small deletions and insertions are either neutral, deleterious or lethal. While it is possible that mutations at this level may confer selective advantage, and that point mutations in regulatory genes may have major developmental effects (see Figure 2a),[25], the generation of new genetic information requires more dramatic changes. The results of most experiments in which populations are mutagenised and then selected for specific mutant phenotypes over many generations demonstrate that there are limits to the extent of change that is possible, and that in general selective pressures tend to be normalising. In other words, even under intensive selection populations tend to retain or revert to the original phenotype. Such small, random mutations are apparently unable to generate new genetic information in experimental terms[6].

## Gene duplication - how to make more genes

It is possible during DNA replication for a single gene to be copied twice, indeed for some genes this is a normal step in their expression[7]. Unequal crossing over in meiosis is a further mechanism which may give rise to gene duplication (see below). As illustrated in Figure 2b, if both copies of the gene are retained, while one must remain functional, and be conserved, the other may be mutated and become non-functional without reducing the fitness of the organism. As the mutated gene 'drifts' it may eventually acquire a new function with selective advantage to the organism and be fixed in the population, thus adding to the genome's informational complexity. All genomes of higher organisms contain families of genes that are structurally related in such a way as to suggest that they arose by this mechanism[8]. Psuedogenes may also arise in this way, being non-functional genes which are clearly related to a functional gene or gene family in sequence and organisation, but which cannot be expressed. Pseudogenes may be seen as a source of genetic variation with considerable evolutionary potential[9].



*point mutation*
- a base change
small deletion or
insertion in one
daughter chromosome
during replication.

*gene duplication*
- copied twice in
replication.

- one gene copy (B)
is now free to
evolve.
A is conserved
by selection.

*homologous but*
*unequal crossing-over*
- in meiosis each progeny
chromosome normally
retains a full set
of genes, of assorted
maternal or paternal
origin.
- here one chromosome
has been expanded (1)
and one contracted (2)
(1) has gained more
information.

*Figure 2. Mechanisms for genetic change.* In each diagram a line ____ represents a gene or group of genes; boxed sections are flanking regions of DNA. X, ▼ are point mutations.

Examples of families of related genes are common, and include the genes of important proteins such as globins (Figure 3), immunoglobulins (Figure 4) and actins, as well as those for the RNA molecules involved in the translation machinery. Immunoglobulin (antibody) genes are particularly important in evolutionary terms, because it is maintained that all antibody genes, and indeed the genes for many components of the immune system, are derived from a single ancestral immune response gene by duplications and mutation. The arguments in favour of this interpretation are very compelling, because it is clear that duplication and mutation of any existing immunoglobulin gene would be potentially advantageous since this would increase the repertoire of the immune system. Indeed in normal lymphocytes immunoglobulin genes are first rearranged and then mutated by specific enzymes which exist to increase diversity

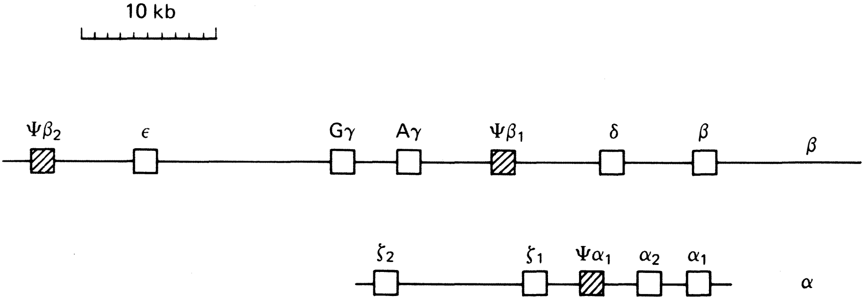


*Figure 3. Organisation of the two families of globin genes.* Every haemoglobin molecule contains four polypeptide chains of the type $\alpha_2\beta_2$, but the $\alpha$-like and $\beta$-like genes differ at different stages of growth e.g. foetus = $\alpha_2\gamma_2$, but adult = $\alpha_2\beta_2$. All the globin genes are similar (homologous) in sequence.

Genes are shown as boxes. Non-functional pseudogenes (e.g. $\psi\beta_1$) are shaded. The scale at top left shows 10 kb of DNA (i.e. 10,000 nucleotide pairs).

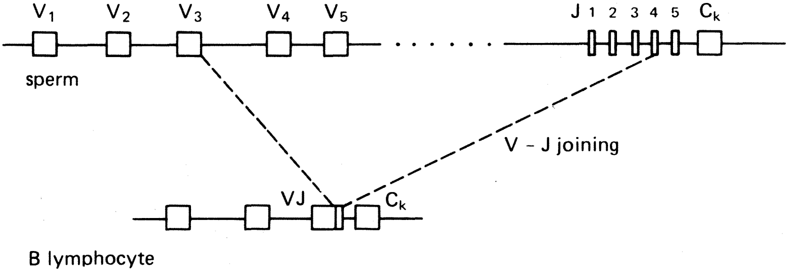


*Figure 4. Immunoglobulin gene rearrangement (light chains).* During B lymphocyte (antibody producing cells) development, a functional gene is formed by joining one of a large number of V (variable) region genes to one of a small number of J (joining) region genes next to a single c (constant) region gene. The DNA in between V and J is deleted. Subsequently the VJ region of the DNA is mutated to increase variability in the antibody proteins. Many V genes are pseudogenes.

and thus to enhance the efficiency of the immune system[10]. It is probable that immunoglobulin gene families, which contain many pseudogenes, do evolve by this mechanism, but to explain the origin of the entire immune system in this way is in clear conflict with the creation of a complete organism with a functional immune system.

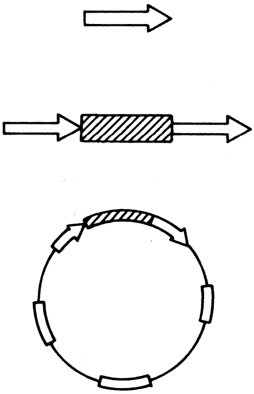
### Recombination — mixing up genes.

The mechanisms that exist in germ cells to maintain genetic variation by assorting the gene complements of homolgous chromosomes in meisosis also present opportunities for generating new genetic information. Aberrant processes such as unequal crossing-over and gene conversion (which could also function as a sort of proof-reading system for maintaining uniformity within certain gene families) may join together segments of different genes to yield a chimeric gene, or give rise to gene duplication (Figure 2c). The evolutionary potential of such events is as described above, and examples of chimeric genes do exist.[11]. Gene conversions has been invoked as an explanation of the coincidental evolution of gene families in which many identical copies are conserved over evolutionary time — a mechanism for resisting change by inducing change!

Specific recombination mechanisms exist in some somatic cells also as a means of generating diversity, including the rearrangement of antibody genes in lymphocytes[10] and the variation in surface antigens of trypanosomes[10(b)], which is a mechanism for evading the immune response. Figure 4 illustrates the rearrangement of immunoglobulin genes.

### Mobile genetic elements — moving genes

Bacteria in particular, and higher organisms as well, contain many small pieces of DNA (insertion sequences, transposons) which may be independently replicated (plasmids, episomes, viruses) and which are able to integrate into and be exised from the chromosome, either at specific sites or at random. Figure 5 illustrates some bacterial mobile elements. Such DNA elements often pick up fragments of chromosomal DNA and can then transfer them to different positions in the genome, to a different cell, and perhaps to a different species. Mobile elements in higher organisms mediate a number of normal cellular processes, including the quasi-inheritable serotype switching in trypanosomes already mentioned. Other examples are the mobile elements which control a wide variety of genetic loci in maize, mating type switches in yeast, and *copia* elements in Drosophilia[12]. As well as controlling essential genetic processes, mobile elements in the genome have been implicated as causes of cancer and other diseases, and sequences transposed by mobile elements are often subject



*Insertion elements* (IS) are able to integrate into and be excised from the chromosome.

When IS pick up a structural gene or regulatory DNA from the chromosome they become *transposons*, which can move DNA segments around the genome.

*Plasmids* are independently replicating genetic elements, often containing transposons, which can be transferred to other cells Antibiotic resistance genes are carried on plasmids.

*Figure 5. Mobile genetic elements in bacteria.* Higher organisms possess similar mechanisms.

to high rates of mutation. In evolutionary terms the ability to transfer genetic material from one organism to another is clearly a powerful mechanism for acquiring new genetic information[13].

Mobile genetic elements also have practical value, and are used in the technology of genetic engineering to investigate the mechanisms of gene expression, and to introduce genes for many medically and commercially valuable protein products into bacteria[14].

## Junk DNA and selfish DNA — evolution's scrapyard?

Bacteria, in general, compete for the resources available in the environment primarily by means of growth rate, and thus it is important to minimise the size of the genome so that DNA replication time is minimised. This probably explains why in simple single cell organisms every base in the DNA has some essential function. In higher organisms, where selection pressures on the genome are more subtle, a large proportion of the DNA has no known function either in coding for, or in controlling the expression of, cellular proteins. Such DNA sequences, which must arise by means of the mechanisms discussed above, are not constrained by any known selective pressures, and are free to evolve independently of the rest of the genome. However, just as a pile of scrapped motor cars contains bits and pieces which are of value to somebody, in evolutionary terms this unwanted collection of DNA sequences is a potential source of new gene functions. This selective potential may be the only selection pressure that maintains such sequences in the genome[15].

## Evolution has a mechanism

This brief survey of normal and aberrant, but experimentally verifiable mechanisms for genetic change, provides clear evidence that evolutionary changes leading to increasing genome complexity can and do occur. It is true that such an increase in complexity has not been demonstrated experimentally, but in many cases it is clearly indicated by generic data, and it is likely that as genetic engineering techniques become more powerful, direct correlations between DNA sequence and novel gene functions will be made[16,17]. Information Theory has also been used to argue against the possibility of novel genetic information arising by random processes, which in a closed system can never result in an increase in the amount of information. It is not clear whether Information Theory is applicable to biological systems in general, but it can certainly be argued the genetic processes are not truly random in the sense required, and that the existence of mobile genetic elements invalidates any concept of an organism as a closed system in informational terms[18].

Evolution has a mechanism. To deny that assertion is to reject a vast amount of valid experimental data.

## Homology — not a process

Evolutionism views all homology — similarities between fossil or living organisms at the morphological or molecular level — as a consequence of common ancestry, and evolutionary trees are constructed on the basis of such relationships. However, as recent debates over the application of cladistics have demonstrated[19], homology tells us about evolution only if evolution is assumed, and more specifically can assist our understanding of evolutionary processes only if an ancestral relationship exists. Nevertheless it is true that evolutionary processes will generate homology at certain levels.

The subject of homology deserves much fuller discussion than is possible in this paper, as it serves as a point of contact between the creation and evolution models. This is because the creationist views homology as a natural consequence of design, and therefore expects to see similarities within and between organisms at every level of structure and complexity. At the same time certain homologies, even if only at the trivial level of those between different breeds of dog, for instance, must be acknowledged to be evolutionary in origin[20].

Both purposeful design and random change, therefore, must be seen as having contributed to the pattern of both diversity and uniformity in the living world.

……

We must now turn to the Biblical assertion that all living things were created mature and complete and perfect by an intelligent, logical and all-powerful designer and maker. What would be the genetic characteristics of such a creation, and what would be the effects upon it of the evolutionary processes we have discussed?

## A 'good' creation — the perfect genome?

Adam, in common with all other living things, was brought forth from the dust of the earth. It is pointless to speculate over the processes used to achieve this, as evolutionists would have us do, because we are not able to understand the mind and the power of God in creation. We may infer that at the end of the creation period, on the evening of the sixth day, there existed a biosphere which was complete and mature, in which every organism was specifically designed and individually created, made to be perfectly adapted to its environment (or vice versa!). While it is possible to speculate about the sizes and characteristics of animal populations, we are told clearly that there was one man and one woman. Because they had not yet sinned the creation was 'very good' and not yet subject to the 'bondage to decay' described by Paul in Romans 8. It was without blemish.

Every structural detail of Adam's physical body, and the genetic information encoding that structure and the development and structure of his descendants, were perfectly adapted to each other and to the environment. Within that environment (Eden) no 'improvement' — new adaptations or increased fitness — was either possible or desirable; only deterioration was possible. We do not know whether Adam was created to live for ever as a physical being — whether indeed he was growing old — but even after the Fall he and many generations to follow lived for a very long time by modern standards. Neither do we know how complex his genome was. It may have been more or less complex than the modern human genome, and it may have contained selfish DNA, pseudogenes and moblie genetic elements as long as these compnents could have no deleterious effects. In other words, Adam's genome may have been created with the genetic potential for evolution, but without having itself evolved; we do not know.

We may also speculate about Eve's genome. This is important because in sexually reproducing organisms the level of genetic variation is vastly increased by the combining of two individual genomes from egg and sperm. It is possible to take the view that Eve was 'cloned' from Adam's rib, by analogy with experiments performed on frogs, but the answer cannot be so simple because she must have differed genetically from Adam if only in her X/Y chromosome complement. We might also predict a significant level of allelic variation between their two genomes, which would eventually generate by recombination, without any need for mutation, a vast amount of diversity within the human population. This would be true of all species, and it is consistent with our understanding of God, who would surely rejoice in the diversity of His creation.

## Fall . . .

The origin of evolution in the sense in which it is understood today, as a process of random change, is concisely summarised in the words of Romans 8, 20, 'the creation was subjected to futility' (RSV). It has not always been subject to futility, but 'lost its purpose' (Romans 8. 20, Good News Bible). The implication of this statement for biology and genetics is that for a period of time the creation was not at the mercy of random processes leading to corruption and death, but that such processes were restrained, either inherently by the genetic make-up of life, or externally by the power of God. The Fall of Adam from grace brought a curse on man, on the ground, and on all creation (Genesis 3.14-19). Through His Word, by an Act of God, the Creator subjected His good Creation to futility — to Evolution. Our use of the word here does not include all that is implied by Evolutionism, but does not exclude anything of evolutionary process.

## . . . and decline

It has already been argued that the only posible effects of genetic change on a good creation would be deleterious. Thus any mutation events in the genome would tend to impair gene function or to subvert normal genetic processes to modify genome organisation and impair gene regulation. The major source of the classical ingredients of neo-Darwinian evolution, mutation and natural selection, is the environment. Normal cellular mechanisms in some cases induce mutation, but these operate only in somatic cells. The germline (hereditary DNA) is subject to copying errors in DNA replication, which at a frequency of 1 in $10^{10}$ to 1 in $10^9$ contribute a negligible amount of genetic diversity. However, in addition aberrant recombination events in germ cells during meiosis may give rise to gene duplication, as we have seen, but subsequent mutation is required in order to generate new gene functions. All cells, germline and somatic, are subject to environmental mutagenesis, which is mediated by chemical mutagens and by a vast spectrum of ionising radiations, all of which cause random genetic damage.

The Garden of Eden was a special, protected environment, and we are not told anything about the state of the world outside Eden prior to the Fall. However, when Adam and Eve were cast out of Eden they were thrust into a harsh environment filled with spiritual and material pollution, violent death and competition. Their new habitat provided selection pressure to accept or reject the mutation which it also induced. Populations increased rapidly and evolution was well under way. In the initial small populations many deleterious mutations must have become fixed, but if the fitness of the human genome is judged in terms of fertility and lifespan, little deterioration in the human gene pool was apparent before the time of Noah.

The environmental impact of the Flood (Genesis 6-9) must have been greater, in quantitative terms, than that of the Fall. All surviving terrestial species passed through a population bottleneck which would have a major effect on gene pools which were already accumulating deleterious mutations. The following factors may be considered as contributing to the first major 'punctuation' of the relative equilibrium of antediluvian life.

1. Inbreeding within small populations results in the fixation of many deleterious mutations and in the human population a consequent increase in genetic load (discussed more fully later)[21].
2. The extreme environments generated by the Flood and radiative movements of animals into them produced correspondingly extreme selection pressures and maintained small breeding populations for a long period. Many speciation events would result.
3. The 'Canopy Theory' proposes that the waters of the Firmament which contributed to the floodwaters had previously formed a protective canopy shielding the earth's surface from a great deal of ionising radiation. The removal of this canopy would increase the rate of radiation-induced mutation and fuel the evolutionary processes[22].

The conditions resulting from the Flood are therefore those which favour speciation in the conventional evolutionary model — genetic drift in small geographically isolated populations leading to reproductive isolation and hence speciation. It can be argued that the pattern of diversity arising within created kinds in a relatively short time under such conditions is comparable to the diversity resulting from evolution from a common ancestor over the vast time-scales required by neo-Darwinian evolution. The time-scale requirements for the two models differ because of the different initial conditions and the direction of evolutionary change required.

## Evolution — which way?

While neo-Darwinian evolution proceeds from a single ancestral species in the direction of increasing genome complexity, creation begins with an (unknown) number of complex genomes, each of which evolves independently (although in competition). The direction of change is indeterminate, as no increase in genome informational content is required, but diversity within kinds must increase. Genetic barriers prevent interbreeding between kinds, but convergent

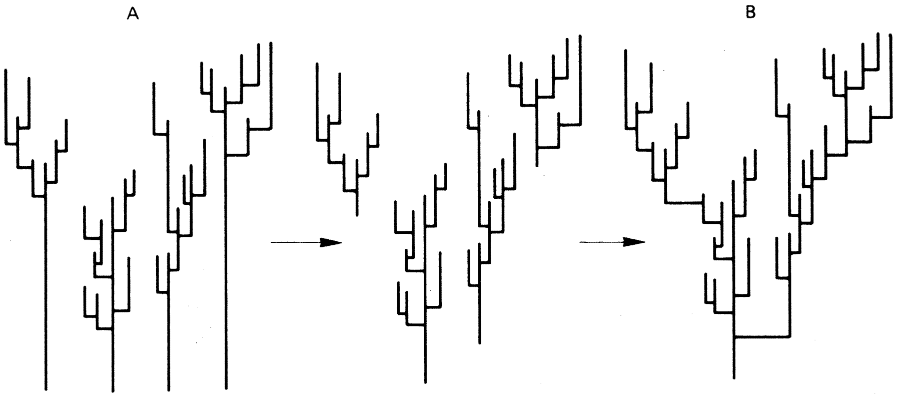


*Figure 6. Hypothetical evolutionary trees.* The vertical axis represents time (scales may differ) while the horizontal axis corresponds to morphology, DNA sequence or other aspects of variation.
A - creation model. B - evolution model.

The data (fossils, DNA sequence, etc.) are incomplete (centre). Scripture reveals that the pattern consists of many trees each rooted in a created kind. Rejection of this requires that different trees be connected by transitions horizontally and be rooted in a common ancestor. In each model the mechanisms for genetic change are identical[26].

evolution may blur distinctions between kinds. Figure 6 illustrates the way in which the two models affect our interpretation of evolutionary trees, and shows how either model adequately explains the patterns of diversity found within the fossil record and within modern species.

It must now be apparent that the argument with evolutionists is not really about process, but about ancestry — primordial blob vs. mature kinds — and about the direction of evolutionary change — 'up' or 'down' or sideways. Much of the debate will continue to centre on the fossil record, which is admittedly difficult to reconcile with the creation model, but at the level of evolutionary processes, the argument is strongly in favour of creation. It is time to look at the evolution of created genomes.

## The evolved gene — evidence of design?

Before looking for evidence of change it is relevant to ask whether evidences of the perfection of originally created genes are discernible in modern evolved genomes. At a detailed level it is impossible to answer this question, but the old 'argument from design' is still valid at the molecular level. In the light of our earlier consideration of the feasibility of a chemical origin of life, the most powerful argument for the creation of genes is that genes exist, and that even the simplest organisms utilise the sophisticated gene expression mechanism found in higher organisms. There remains no trace of any putative primitive gene expression system or of any biological information system simpler than that which is ubiquitous in modern organisms. The design argument also includes the question of homology, discussed earlier.

A full understanding of molecular homology requires knowledge of the constraints on protein structure, and thus amino acid sequence, which determine whether a protein molecule will perform a given function. These constraints vary, since certain functions may be performed by a wide range of protein structures, while others show very little variation over a wide range of species. Thus the amino acid sequence (and therefore the gene coding region) of histone Hl is very highly conserved across all eukaryotic species, indicating that only a very narrow range of structures is able to carry out its very specific function in binding to DNA in the chromatin. This in itself tells us nothing about the origin of the gene, or of species. Likewise the amino acid sequence of cytochrome c has been found to show much greater variation, and the structure is clearly less constrained. The evolutionary trees which are constructed from such molecular data may be treated in the way described in Figure 6. However, there are fundamental differences in interpretation between the two models. In the evolution model, all similarities are a consequence of common ancestry, while differences are a consequence of divergent evolution, and the main determinant of protein structure, namely functional constraints, is by-passed. In the creation model, similarities result from functional constraints in design, while differences may also be introduced by design to optimise protein function in particular cell environments. Further differences will then arise from evolutionary divergence, the extent of which will be limited by functional constraints (as it is in the evolutionary model also).

Therefore, although we may determine which features of protein structures are highly conserved and therefore functionally indispensable, it is impossible to predict optimal structures encoded by the hypothetical ‘perfect’ genome. Nevertheless the evolution of created genes adequately explains observed patterns of molecular homology, and is a more realistic framework for interpreting homology on a functional basis[20].

## The evolved gene — gene disorganisation

The changes in gene structure discussed so far have been limited to point mutation in structural genes and the effects of natural selection on modified protein functions. Now we consider the effects of other evolutionary processes, described earlier, on the organisation and expression of created genomes. These effects may include the generation of new genetic information in the ways already described, but are more likely to lead to deleterious effects, either on protein coding sequences or on gene organisation and the control of gene expression. In this section the emphasis will be on deleterious effects.

Pseudogenes may arise by mutation of gene duplication, or from individual members of gene families which become non-functional by mutating without gene duplication. The loss of a member of a gene family would normally be highly disadvantageous, but such events might be tolerated in immunoglobulin gene families, which contain many pseudogenes.

Genes or gene fragments may be moved to new locations in the genome with or without duplication or mutation. One possible consequence of such changes is to bring genes under the control of different controlling element, such as hormonal regulation, and although many such regulatory changes will be deleterious or lethal, some may have evolutionary potential. The best studied examples of changes in gene regulation leading to major phenotypic effects are a group of genes called oncogenes, so named because they are all implicated in causing cancer. Oncogenes are in fact perfectly normal genes whose protein products are involved in the control of cell division and the cell cycle, and many of them are expressed in a cell cycle specific manner. It is when the control of cell division is disrupted by deregulating these genes that they become tumorigenic. This can happen in at least two ways, apart from simple mutation of their regulatory elements. In many lymphomas and leukemias an aberrant immunoglobulin gene rearrangement has brought an 'oncogene' under the control of immunoglobulin gene regulation. These events always also involve a chromosome translocation (see below), and it is probable that very many such aberrant rearrangements take place during lymphocyte differentiation, most of which are never detected because they are lethal to the cell. Only those immortalised as tumours can be observed.

Cancer may also be caused by tumour viruses, and these include retroviruses, many of which contain mutated copies of cellular oncogenes as well as other genes which have been taken out of the genome by various mobile elements. Every mammalian genome appears to contain retrovirus sequences integrated into the genome at high frequency[23]. These, although normally latent, may become activated to become pathogenic or carcinogenic. Virus infection may of course, have similar consequences. Most cancers involve somatic cell types, but similar mechanisms to these may be implicated in teratocarcinomas and in teratogenesis — developmental abnormalities in the embryo — and presumably also affect germline cells.

Chromosome translocations, in which sections of two different chromosomes become joined, would normally be lethal, but are occasionally preserved as tumours, as described above. Translocations can also be carried in the germline and cause a number of inherited defects, as does polyploidy — more than two copies of a chromosome resulting from defective chromosome segregation at mitosis. Again, events such as these are probably frequent but rarely survive[24].

In summary, the effect of evolutionary change will be to move from a highly ordered genome towards one which is less ordered and which, though it may contain additional and novel genetic information, also contains much additional functionless DNA which is potentially a source of new genetic information but also potentially deleterious. This is a fair description of a modern genome and of the general observed direction of change.

## Genetic load — an evolutionary burden

A major genetic problem for the human species, and for many populations of domestic animals, is that in general it is not subject to natural selection; most animal populations are. Thus many deleterious mutations and genetic defects which would normally be eliminated from a population by selective pressures, are retained and propagated. Ironically the problem is exacerbated by modern medicine, which as it seeks, rightly, to treat a wide range of genetically inherited diseases, also succeeds in increasing the incidence of those disorders and of the defective genes which cause them. For instance, since the discovery of insulin the incidence of childhood diabetes, and the lifespan and fertility of diabetics, have been increasing steadily, along with the frequency of those HLA genotypes which are known to dispose individuals to diabetes. This is particularly true in the Western world, but such paradoxes occur in less developed nations as a consequence of natural selection. The sickle cell trait, a severely debilitating disease caused by a mutant globin gene, is very common in certain areas of Africa because the defective red blood cells which characterise the trait are resistant to the malaria parasite[27].

Genetic load is perhaps the clearest indication of the direction in which evolution normally proceeds. Its effects can be measured over periods of years at present, but can be traced back in Biblical history to the early chapters of Genesis. It can be argued that the decline in human lifespan following the Flood, from 950 years (Noah) to 175 years (Abraham — a good old age), is correlated with increasing genetic load resulting from 1) inbreeding and 2) rapid evolution of the human gene pool[28]. The somewhat simplistic reasoning assumes that death occurs when the residual genetic information in the organism is no longer sufficient to overcome the Second Law of Thermodynamics. From conception, the inherited genetic information in all the cells of the organism is being slowly degraded, and this certainly contributes to the ageing process. If the fertilised egg begins its development with a significant mutational burden, ageing will be more rapid and death correspondingly sooner.

However, the genetic basis of ageing is unclear. Recent work on animal tissue culture cells has suggested the idea of 'programmed senescence', because it appears that animal cells (more accuractely, cell lineages) are genetically programmed to die after a fixed number of cell divisions. It is not clear whether this property is true of the same cells in their normal environment *in vivo*, and it is possible also that senescence is related to genetic load, but there are instances in which cell death must be seen as a normal and essential differentiation event in particular cell lineages[29]. We may speculate as to whether programmed senescence is a consequence of evolution or a more specific aspect of the Curse. Whatever the genetic basis, the effect is summarised in Genesis 2.17b, 'dying you shall die.'

……

## Ambiguities

The argument in this paper has been in very general terms. It will be apparent that any attempt to study the origin of a particular gene comes to the conclusion that the evidence is consistent with either of the two models. In the view of the author the only soundly based exception to this is that of chemical origins. In any other detail the evidence of science is ambiguous, and we should be wary of the temptation to argue from science to Scripture. Our entire presentation of the Creation model must begin with Scripture, or it will fail. Equally, scientific ignorance or unsoundness will not honour the Creator and will deviate from the truth.

## Notes and references

1 The aim of this paper is to suggest ways in which demonstrable genetic mechanisms for evolutionary change are consistent with the creationist model of origins. The genetic processes discussed are highly technical and are given in simplified terms. Only minimal references to research articles and reviews will be given, and for ease of access most are from the Journal *Nature*; more will be found in any standard text on molecular evolution, although it must be recognised that all such texts are committed to an evolutionistic view of genetics as the basis of interpretation *and* description of genetic processes. For a recent creationist view of mutation see Leslie, J.G. *Ex Nihilo* Vol.6 No.4, pp. 38-45.

2 For a fuller treatment of chemical evolution, see Wilder-Smith, A.E. *The creation of life: a cybernetic approach to evolution.* Harold Shaw, Wheaton, Illinois (1970); Peet, J.H.J. *Thinking again about the origin of life.* Biblical Creation Society (1983); Gish, D. *Speculations and experiments on the origin of life.* Institute for Creation Research (1975).

3 Because of the small generation times of bacteria, mutation events occurring at frequency of 1 in $10^8$ cells or less can be detected. When phenotypes such as antibiotic resistance, or ability to use hydrocarbons as a carbon source, may be selected from populations originating from a single cell (which lacked the selected phenotype), with a genome size of $10^6$-$10^7$ base pairs of DNA, it is not possible that previously existing genetic information is being selected. It therefore appeared by evolutionary processes.

4 It is, however, significant that no 'speciation' event has been documented after years of such experiments with bacteria (see above). Experiments with Drosophila involving mutagenesis and selection over many generations have demonstrated that most selection is normalising, and populations tend to retain or to revert to the original phenotype.

5 For a good review, with further references, see Hunkapillar, T. et al. *The impact of modern genetics on evolutionary theory.* (1982). In *Perspectives on evolution,* ed. R. Milkman, Sinauer Associates, pp 164-198.

6 It appears that in protein sequences regarded as evolving on accepted evolutionary pathways, the frequency of deletion events exceeds that of insertions (de Jong, W.W. & Ryden, L. *Nature, 290, 157* (1981)). The implication is that proteins become smaller as they evolve!

7 Chisholm, R. *Gene amplification during devolopment* (1982) Trends in Biochemical Sciences, *7* 1-2.

8 The genes for ribosomal RNA and transfer RNA are further important examples of gene families, with problems for both the creation and evolution models. See Jeffreys, A.J. and Harris, S. *Processes of gene duplication. Nature (News & Views) 296, 9 (1982)* Dover, G. and Coen, E. *Nature (News & Views) 290, 731* (1981).

9 Li, W. et al. *Pseudogenes as a paradigm of neutral evolution. Nature 292, 237* (1981).

10 For reviews of antibody gene organisation and expression see (a) Tonegawa, S. *Nature, 302, 575* (1983); (b) Robertson, M. *Nature (News & Views) 297, 184* (1982).

11 For example, chimeras of haemoglobins and of immunoglobin isotypes exist in man and mouse. Whether such events have given rise to novel protein functions in evolution is a matter of speculation. The point is that the mechanism exists and such recombination events do occur and may be stably inherited.

12 For reviews, see Bishop, J.M. *Ann. Rev. Biochem. 47, 35-88 (on retroviruses)* (1978); Bukhari, A.I., Shapiro, J.A., Adhya, S. *DNA insertion elements, plasmids and episomes.* Cold Spring Harbor Laboratory, C.S.H. New York (1977); Naevers, P. & Saedler, H. *Nature 268, 109-115* (1977).

13 Transposition of regulatory DNA sequences will also have major phenotypic effects. An entire set of genes may be brought under the control of a different regulator gene, or of a hormone. Events of this type are implicated in certain cancers and in other diseases. The oncogenic bacterium, *A. tumefaciens*, is able to cause tumours in plants because it carries a large plasmid ($T_i$) which transfects and then transforms plant cells into tumour cells.

14 *E. Coli* bacteria have been engineered to synthesise human insulin, growth hormone, interferon, and other expensive products with medical or commercial value.

15 For a summary of ideas on selfish DNA see short articles by Orgel, Crick & Sapienza; Dover & Doolittle; Jain, in *Nature 288, 645-648* (1980). Selfish genes have also been discussed in relation to sociology and politics. For an example see letter by Dawkins, *Nature, 289, 528* (1981).

16 In bacteria such correlations can already be demonstrated.

17 Interspecies and intraspecies homologies at the molecular level are often compellingly consistent with derivation from common ancestors by the mechanisms described. At this level, the evolution model is very consistent with the facts. However, see notes on homology below.

18 It is possible to build computer models of gene expression by viewing DNA as a machine code. Such models are inadequate, partly because the genome is a digital information system, whereas the expression machinery and the resulting phenotype are analogue systems. We simply do not know the rules, and it is certain also that biological information violates the rules of Information Theory.

19 Patterson, C. *Cladistics and Classification*. New Scientist, p. 303, 29 April 1982.

20 The example given here (dog kind) is actually trivial, because it is small differences between breeds that are significant at the genetic level. However, molecular homology is a point of contact between creation and evolution because in the final (or present) product, the structure or genotype, whether designed or evolved (or both), is constrained by the function or phenotype to which it is now adapted. (This explains why evolutionists often find themselves describing evolutionary events in telelogical terms — e.g. David Attenborough, Life on Earth, BBC TV). Consequently it is not possible, in principle, to determine whether a particular feature of homology results from design or from evolutionary adaptation of an ancestral feature, without making an assumption. This problem applies less to DNA sequences, which are less constrained than protein sequences because of redundancy in the genetic code. A detailed analysis of codon usage, which varies in specific ways from organism to organism and from protein to protein, might allow the development of rules which could distinguish design and ancestry.

21 Inbreeding was later outlawed in the Law of Moses, for sound genetic reasons.

22 The writer does not subscribe to Flood Geology, and is unconvinced by the arguments for the canopy theory. The implications for evolution are nevertheless worth considering.

23 About 0.1% ($3 \times 10^6$ base pairs) of the mouse genome is probably derived from retrovirus sequences. Many such mobile elements probably parasitise the mammalian genome.

24 Many chromosome translocations, some with major developmental effects, have been characterised in Drosophila, which seems to tolerate such changes remarkably well, as many such mutants are viable in natural populations. In mammals most translocations are lethal or associated with major developmental or physiological defects.

25 There are instances in which a small mutation event in even a structural gene may have major, developmental effects. The *unc*54 mutation in the nematode worm, *C. elegans*, is a behavioural mutant which results from incomplete development of the nervous system. The genetic lesion is a pathway of a cell lineage in the developing nervous system (Brenner, unpublished). The change is in the opposite direction to that required for 'upward' evolution (increasing complexity), and would need to be reversed (a highly improbable event) to generate a mobile worm from an immobile, but viable one. Nevertheless the amount of genetic change required to achieve such a major evolutionary step is small.

26 a) The form in which Figure 2b is drawn is not intended to imply a particular mode of evolution (gradualism or punctuation).

b) In both models there are uncertainties concerning timescales, the nature of created kinds, transitional forms, etc. Note, however, that in the creation model, the extent of change is constrained by the rate of change and by time since creation. In evolution the timescale is constrained, by the rate of change and by the total extent of evolution required. It is not my purpose to discuss the fossil record, which is crucial here, and which has its own problems for both creation and evolution.

c) Model A implies nothing about the 'direction' of evolution; B requires a progression from simple to complex.

27 Strangely, this phenomenon is oft quoted as an example of evolutionary progress. However, despite a marginal selective advantage — individuals with sickle trait are less likely to die of malaria — it is clear that the inherent fitness of sickle genomes is lower than non-sickle. Sickle cell trait results from the heterozygous condition (one copy of the HbS gene). Homozygosity (both genes HbS) is severely debilitating or fatal. Moreover, there is no increase in genome complexity.

28 Dietary changes also followed the Flood (Genesis 9.3).

29 In the study of cell lineages in nematodes[25], it is found that some lineages progress by division of a cell into two different daughter cells, one of which differentiates further while the other *invariably* dies. This cell death, which follows division, must be genetically determined. It could be caused negatively, by a specific genetic defect induced at cell division, or positively, by inducing a gene for an intracellular toxin, for instance. Some fully differentiated cells (e.g. red blood cells) die because the DNA is degraded at a specific stage in their development.

# CORRESPONDENCE

Dear Sir,

'Creationism needs Catastrophism'

I read with interest the article above by Graham Fisher. In this he pleads for better evidence that will support the 'young earth' model. He notes that the evidence of geology is difficult to reconcile with one great Flood (p.12). He also mentions that a major feature of the Flood is the breaking up of the fountains of the deep which must have had a great effect upon the geological layers. The impact of an asteroid is suggested as the cause of the Flood.

What is very surprising to me is that with all these suggestions that Fisher makes, not once does he refer to the work of Barry Setterfield who has produced evidence for a model that answers all these problems in a very thorough manner. I can only presume that he has never heard of this new development even though it was first published some three years ago. I am of course referring to the subjects of 'The decrease in the speed of light' and 'The Tilt of the Earth's Axis' which Setterfield has researched in great detail.

For example, he has quoted the geological discovery that rock material, clays and other sedimentary deposits can be precipitated very rapidly from CHEMICAL solutions in hot supercritical water that would have flowed from the depth of the earth when the fountains of the deep were broken up. This solves a major problem for 'young earth' creationists. Also, there is now good evidence from ancient astronomical records that the earth was sharply tilted around the year 2345 B.C. — the date of the Flood. The most likely cause was that the earth was struck by an asteroid.

May I suggest that these subjects be brought to the attention of the members so that they may be examined and improved upon. If established, they will provide a reliable scientific scenario that fully supports those of us who believe the earth was created 6,000 years ago in 6 days.

Yours sincerely,

Malcolm Bowden.

# ROCK STRATA and the GEOLOGICAL COLUMN

## David Watts

Most commonly the term Geological Column is applied to a composite columnar vertical section in which there is an attempt to represent superimposed sedimentary rock strata in their relative time order for the earth as a whole. In this way it is thought the Column can be used as a central reference, in relation to which a large part of the vast fund of geological information and theory can be organised.

The major subdivisions of the Column are called rock systems, and two progressively finer sub-divisions are termed respectively: series and stages. Corresponding to these rock units are units of relative geological time. These are termed respectively: Periods, Epochs and Ages. Thus we have the well-known names for the periods of geohistory: Cambrian, Ordovician, Silurian, Devonian, etc..

In published versions of the Geological Column, quantitative time spans — usually in millions of years — are often associated with each of the geological periods. However the assignment of quantitative time is made on the basis of principles[1,2] quite distinct from those used to establish the relative time sequence of the rock strata constituting the Geological Column. It is a major aim of this paper to clarify this important distinction between (1) the Geological Column as a genuine sequence of global rock strata and (2) the cumulative quantitative time span of 0.6 BY commonly assigned for the formation of all these rock strata. Where this distinction is recognised the way is opened for a reappraisal of the problems of geohistory. The approach differs, at least potentially, from the prevailing concensus in academic geology today in that it is prepared to probe and question the validity of current estimates of the age of the earth. However, we do not necessarily affirm that these estimates are radically incorrect. In this respect and in our acceptance of the general validity of the Geological Column we also differ from those radical critics of current geology who strive to interpret virtually all fossiliferous rocks as products of one year of global catastrophism in the geologically recent past. But what is the basis for acceptance of the Geological Column as a genuine sequence of strata? This question can be approached by consideration of the principles of stratigraphy used for ordering rock strata and then the way that these principles have been applied during the past 250 years in the recognition and naming of rock systems and the associated periods of relative geological time. The order of magnitude of time that may have elapsed during the formation of all the rock strata is a subject that can be discussed subsequently.

## Principles for ordering rock strata

The study of earth history has been developed chiefly on the basis of the distribution, structure and composition of continental rocks . A relative sequence of geological events has been worked out on the basis of three empirically-based principles. These are concerned with the recognition of geometrical relationships between rock strata in the field. Exceptions to these principles will be discussed later.

1. *The principle of superposition* states that: In any *undisturbed* stack of layered sedimentary or volcanic rocks the layer which is at the bottom of the pile must be *older* (i.e. deposited earlier than the layer immediately above it).

2. *The principle of cross-cutting relationships* states that: Any body of (igneous) rock, whose borders transect that layering or other structures in surrounding rocks, was emplaced in its present position *later* than the surrounding rocks (i.e. rocks that cut across others are relatively younger).

3. *The principle of faunal succession* states that: In general, it is possible to determine the *relative* age of a given layer of fossil-bearing sedimentary rocks on the basis of the fossil plants and animals which it contains. It should be noted that this principle is quite independent of the validity or invalidity of the theory of organic evolution.

## The recognition and naming of rock systems

As early as the middle of the eighteenth century, Italian and German geologists had classified their local rocks into three groups: *Primary* (rocks like granite and gneiss, with neither layering nor fossils), *Secondary* (cemented sedimentary rocks, generally exposed in the mountains), and *Tertiary* (weakly consolidated sedimentary rocks of the lowlands, which rested upon the secondary rocks).

In the early nineteenth century, William Smith, a land surveyor, produced a geological map of England and parts of Wales and Scotland. In the area mapped by Smith and his early followers, the oldest strata were grouped as the Old Red Sandstone. These are exposed, for example, in parts of Scotland and in Devonshire and are considered a part of the *Devonian* System. Resting on the Old Red Sandstone is a group of strata called by Smith the Mountain Limestone and these in turn are overlain by the rocks of the Coal Measures. These rocks and the underlying Mountain Limestone are now grouped together as the *Carboniferous* system. Above the Coal Measures, Smith recognised a series of beds called the Magnesian Limestone, followed in turn by the New Red Sandstone. Both these formations contain few fossils and appear to be largely of continental rather than marine origin. The Magnesian Limestone is now considered part of the *Permian* System, named from a province in Russia just west of the Ural mountains, where marine fossiliferous rocks occupy a similar stratigraphic position. The New Red Sandstone, on similar grounds, is now regarded as part of the *Triassic* System, named from the three (triad) formations that are found just above the Permian System in Germany. Overlying the New Red Sandstone is a series of richly fossiliferous beds which Smith divided into many formations. Some years later, many identical fossils were found in the rocks of the Jura Mountains of Switzerland and France, whence the *Jurassic* System derives its name. Towards London, the Jurassic strata are overlain by greensand, and this in turn by chalk. This series is grouped as the *Cretaceous* System (from the Greek word for chalk). The fossils present are identical to those in the Lower Chalk of the Paris Basin, which is also underlain by Jurassic rocks.

Overlying the cretaceous chalk, Smith found the London Clay, a group of beds rich in fossils like those in the beds above the chalk of the Paris Basin. These beds, both in England and France, are now regarded as part of the *Tertiary* System, a name that has survived from the classification of the eighteenth century. The diverse gravels, sands and other alluvial and glacial deposits above the Tertiary and below the obviously sub-recent deposits were classified by William Buckland as a discrete geological unit, subsequently renamed the *Pleistocene* epoch of the *Quaternary* period.

More than a generation after Smith, the stratigraphy of the highly disturbed rocks below his Old Red Sandstone was worked out. Three new systems were recognised: in descending order *Siberian*, *Ordovician* (both names of Old British tribes) and *Cambrian*. The Cambrian strata are the oldest rocks that contain fossils in any abundance, although sedimentary rocks thousands of feet thick are found beneath them in some regions. Adam Sedgwick clarified the stratigraphy of these lower palaeozoic rocks, working from the base of the sequence upwards. He disentangled the Cambrian system in North Wales entirely without the use of fossils. Meanwhile Roderick Murchison went to South Wales and worked from the top of the sequence down.

It is apparent from this outline, that the initial discovery of the sequence of ten super-imposed rock systems from Cambrian to Tertiary was *not* based upon the observation at one place of deep canyons cutting into highly upheaved horizontal strata. None exist in the British Isles. Rather, strata have been exposed as a result of differential movement and tilting of rocks, followed by erosion uncovering older strata particularly in mountainous areas. As a result of such tilting and other movements great surfaces of dipping but undoubtedly normally superimposed strata are now found at or near the surface and are therefore accessible to the geologist. These bear witness to a relative time sequence of geological events, which is valid irrespective of the magnitude of the time period required for the formation of each rock system.

## The Standard Geological Column

Following the recognition of the existence of the Cambrian to Quaternary sedimentary strata in Britain and Western Europe, the resultant Standard Geological Column has become the basis for comparison with other rock strata exposed elsewhere in the earth's crust. This leads us to consider four major issues:

1. The global distribution of sedimentary rocks.
2. The question of lateral (inter-continental) correlation of rock systems.
3. The interpretation of 'out of sequence' strata.
4. The question of gaps in the standard geological column.

### 1. The global distribution of sedimentary rocks

Approximately two-thirds of the total land area of the planet is blanketed by many layers of sediments, commonly transformed into stratified rock[3]. However, this does not mean that there is evidence of ten rock systems as successive 'onion skins' around the globe, i.e. *continuous* over the continents. Direct knowledge of a given rock system, in the crustal rocks of a given locality, can only be obtained from either surface exposures or borehole core analysis. However world outcrop areas of geologic periods seem to decline exponentially when going stratigraphically downwards, as would be expected. Moreover the lateral extent of given rock systems will vary because of the space-time zones of non-deposition and also because of rock erosion subsequent to deposition.

An estimate of the global distribution of rock systems has been made by Woodmorappe[4], based on the work of the Soviet geologist Ronov, and others. He finds that nearly 13% of the earth's land *surface* has five geological periods (rock systems) represented; out of 10, slightly less than 1% has all 10 periods simultaneously in place.

### 2. Inter-continental correlation of rock systems

The original divisions of the geological column into rock systems were based on geometrical or stratigraphical relationships between locally and regionally exposed strata. Fossils played a secondary rôle. However, correlations of distant strata cannot be based upon geometrical considerations and are made instead by comparison of the assemblage of fossils contained in the rocks. The most suitable fossils for correlation over wide areas are those of abundant free-swimming or drifting ocean organisms. Assuming an analogy between past and present types of sedimentary environment, it is important to keep in mind the limitations to the spread of organisms imposed by their natural habitats. The term *facies fossil* is generally used for a group of fossils found only in a particular kind of sediment;

for example, a 'limestone-reef facies'. In his stimulating and provocative volume: *The Nature of the Stratigraphical Record*, Derek Ager commences with a chapter on the evidence for the prevalence over vast areas of the earth's surface of such specific types of sedimentary environment at certain times in geohistory. Such past environments are revealed through the presence of facies fossils.

As a trans-Atlantic example of inter-continental correlation, we may compare the stratigraphy of Tennessee, Alabama and Georgia in the United States with the geology of the Paris Basin of France and the Ardennes Massif in Belgium. When we look at the succession of rocks from the centre of the Paris Basin, north-east to Charleroi in Belgium, the cretaceous strata of the Paris Basin unconformably overlie the folded Palaeozoic strata of the Ardennes. But successively older rocks: Jurassic and Triassic appear in the Paris Basin, above the unconformity surface, further to the south-east of this section. Similarly across the Atlantic in the Gulf coastal plain of south-east USA, boreholes show that there is a succession of Upper Mesozoic and Caenozoic strata, which parallel those of the Paris Basin, and which overlie the folded Palaeozoic rocks of the Appalachians. Moreover there are both structural and faunal parallels between the Palaeozoic rocks of the Ardennes and Appalachians. Consequently in both these areas, the following broad outline of geological events seems to hold in common:

1. Sedimentation during 'Palaeozoic time'.
2. Folding, mountain-building and erosion at or towards the end of this era.
3. Renewed sedimentation in at least part of these areas in 'Mesozoic and Caenozoic times'.

The same broad pattern of strata obtain in Europe, in America, in Asia, Africa and Australia. Correlations of strata occur across all these continental regions.

### 3. The Interpretation of 'out of sequence' strata

For many critics of the validity of the Geological Column, a seemingly convincing argument is the occurrence of 'out of sequence' strata. These are instances where rocks, classified on the basis of fossil content, are found with 'older' strata superimposed upon 'younger' strata. The conventional explanation is that the 'older' rocks are indeed older and they have been overthrust upon the younger rocks subsequent to their initial consolidation. These overthrust strata are often termed nappes. The interpretation of Alpine structures in terms of nappes began in 1841, when Escher van der Linth announced his discovery of overthrusting in the district south of Glarus in Switzerland . He described the highly spectacular occurrence of *Verrucano* (a thick Permian formation) over light-coloured

Mesozoic and Tertiary beds. He thought of the structure in the simplest possible way as two giant recumbent folds, one overturned towards the south, the other towards the north. Later Marcel Bertrand proposed that, instead of two opposite facing folds, the mechanism that had formed the structure was a single nappe directed from the SSE. This required an overthrust movement of at least 35 km. At the time this was widely regarded as mechanically impossible. The proposal was in seeming conflict with Lyellian geological principles!

Since that time numerous nappe structures have been discovered in regions of the earth's land surface which have been subject to tectonic disturbances, for example, the Moine overthrust in Scotland. Any geologist who holds 'catastrophist' views to any extent should be prepared to consider the possibility of, and the mechanisms for such overthrusting.

In many instances a certain sequence of strata can be followed from a less to a more intensely disturbed area and the dip of the strata observed to increase to and beyond 90° from the original horizontal so that they are then overturned and the sequence of layers inverted. Such 'hinge' zones, in which layers are overturned over 180°, are perfectly visible in some deep alpine valleys; for example, the recumbent folding in the Morcles nappe is visible in the Gasterntal valley, south of the Doldenhorn in the Bernese Oberland. The reverse sequence in which the fossils are found locally, therefore does not invalidate, but on the contrary strengthens their value as stratigraphic markers; because we know from independent tectonic evidence that the layers are there in an overturned position. The same applies when older rock masses are pushed up and over neighbouring areas of younger rock. The overthrust fault plane may be visible at the point of contact and will often be characterised by tectonic criteria related to overriding phenomena.

Critics of overthrusting have continued to argue that certain structures in the Rocky Mountains of western USA could not have been formed by these means. Several contact points have been identified which apparently lack tectonic breccia — broken and crushed rock fragments at the interface. However these critics have not yet demonstrated full and impartial examination of all the field evidence in these regions.

In recent years there has been intense study of such nappe structures in the USA, Norway, Iceland and France. I am indebted to Michael Garton, a professional specialist in such studies, and a member of the BCS, for his advice on recent developments. These include the recognition of 'duplex' structures and the way that repeated small thrusts and thickenings can lead to substantial displacements. *Overthrusts deduced from an analysis of structure often have very little evidence of movement at the fault plane — which may be indistinguishable from a bedding plane.*

An example of a duplex structure occurs at a quarry in France, between Calais and Boulogne, where Devonian rock has been overthrust over Carboniferous limestone. In the USA, Chief Mountain in the Rockies is the site of a duplex structure above the Lewis overthrust. To the east, in the Appalachians there is evidence of very extensive overthrusting. In Norway, extensive nappe areas have been analysed by Morley, Hossack and Garton, for example, in a section just north of Oslo. A similar picture of many repetitions emerges from napping 100 miles further north. The effect of adding up all these repeated small thrusts is to point to a source of these thrust sheets some 400 km to the west in the North Sea area. A new model of overthrusting was proposed in 1983 and is already being successfully applied to major structures throughout the world.

## 4. Gaps in the standard Geological Column

Divisions between rock systems in the standard column are based on abrupt changes in the fossil assemblages of the strata in Europe. These points of division are understood to signify periods of erosion or non-deposition in the European stratigaphic series. As stratigraphic correlations have been extended to other continents, however, inermediate series of strata have been recognised in some of these other regions. Even the gap between the Palaeozoic and Mesozoic eras is apparently bridged by nearly complete successions of beds in Nevada and in the Himalayas. Further research may show whether or not the remaining gaps in the standard column will be bridged by fossiliferous strata.

## References

1. D.B. Kitts. *Geologic Time.* Journal of Geology *74* 127-146 (1966)
2. J.E. O'Rourke. *Pragmatism versus Materialism in Stratigraphy.* American Journal of Science *276,* 47-55 (1976)
3. H. Blatt and R.L. Jones. *Proportions of exposed igneous, metamorphic and sedimentary rocks.* Geological Society of America Bulletin *86,* 1085-1088 (1975)
4. J. Woodmoraffe. *Creation Research Society Quarterly 18,* 46-71 (1981)
5. D. Davis, J. Suppe and F.A. Dahlen. *Mechanics of fold and thrust belts and accretionary wedges.* Journal of Geophysical Research *88,* 1153 (1983)

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